What is claimed is:

1. A method for detecting an association in a population of unrelated individuals between a genetic locus and a quantitative phenotype, wherein two or more alleles occur at the locus, and wherein the phenotype is expressed using a numerical phenotypic value whose range falls within a first numerical limit and a second numerical limit, the method comprising the steps of

a) obtaining the phenotypic value for each individual in the population;

b) determining the minimum number of individuals from the population required for detecting the association using Eq. 2;

c) selecting a first subpopulation of individuals having phenotypic values that are higher than a predetermined lower limit and pooling DNA from the individuals in the first subpopulation to provide an upper pool;

d) selecting a second subpopulation of individuals having phenotypic values that are lower than a predetermined upper limit and pooling DNA from the individuals in the second subpopulation to provide a lower pool;

e) for one or more genetic loci, measuring the frequency of occurrence of each allele at said locus in the upper pool and the lower pool;

f) for a particular genetic locus, measuring the difference in frequency of occurrence of a specified allele between the upper pool and the lower pool; and

g) determining that an association exists if the allele frequency difference between the pools is larger than a predetermined value.

2. The method of claim 1, wherein the difference in frequency of occurrence of the specified allele has associated with it an error of measurement.

3. The method of claim 2, wherein the error of measurement is 0.04.

4. The method of claim 2, wherein the error of measurement is 0.01.

5. The method described in claim 1, wherein the predetermined lower limit is set so that the upper pool ranges from including the highest 37% of the population to including the

highest 19% of the population and the predetermined upper limit is set so that the lower pool ranges from including the lowest 37% of the population to including the lowest 19% of the population.

6. The method of claim 1, wherein the predetermined lower limit is set so that the upper pool includes the highest 27% of the population and the predetermined upper limit is set so that the lower pool includes the lowest 27% of the population.

7. The method of claim 1, wherein the genetic locus has two alleles.

8. The method of claim 1 wherein the population includes individuals who may be classified into classes.

9. The method of claim 8, wherein the classes are based on an age group, gender, race or ethnic origin.

10. The method of claim 8, wherein all the members of a class are included in the pools.

11. The method of claim 1 for determining the genetic basis of disease predisposition.

12. The method of claim 11, wherein the genetic locus which is analyzed for determining the genetic basis of disease predisposition contains a single nucleotide polymorphism.

13. A method for detecting an association in a population of unrelated individuals between a genetic locus and a quantitative phenotype, wherein two or more alleles occur at the locus, and wherein the phenotype is expressed qualitatively as being either affected or unaffected, the method comprising the steps of

a) identifying the phenotype as being either affected or unaffected for each individual in the population;

b) determining the minimum number of individuals from the population required for detecting the association using Eq. 1;

c) pooling all or a portion of the affected individuals into a first pool and all or a portion of the unaffected individuals into a second pool;

d) for one or more genetic loci, measuring the frequency of occurrence of each allele at said locus in the first pool and the second pool;

e) for a particular genetic locus, measuring the difference in frequency of occurrence of a specified allele between the upper pool and the lower pool; and

f) determining that an association exists if the allele frequency difference between the pools is larger than a predetermined value.

14. The method of claim 13, wherein the first pool and second pool have the same number of individuals.

15. The method of claim 13, wherein the difference in frequency of occurrence of the specified allele has associated with it an error of measurement.

16. The method of claim 15, wherein the error of measurement is 0.04.

17. The method of claim 15, wherein the error of measurement is 0.01.

18. The method of claim 13, wherein the genetic locus has two alleles.

19. The method of claim 13, wherein the population includes individuals who may be classified into classes.

20. The method of claim 19, wherein the classes are based on an age group, gender, race or ethnic origin.

21. The method of claim 19, wherein all the members of a class are included in the pools.

22. The method of claim 13 for determining the genetic basis of disease predisposition.

23. The method of claim 22, wherein the genetic locus which is analyzed for determining the genetic basis of disease predisposition contains a single nucleotide polymorphism.